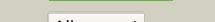
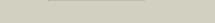
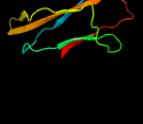
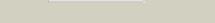
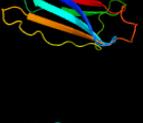
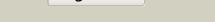
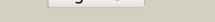
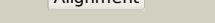
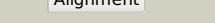
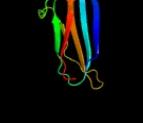
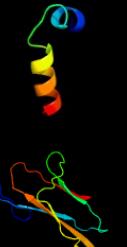
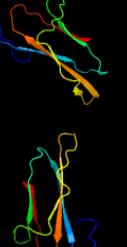
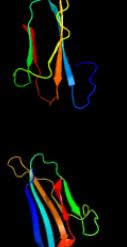
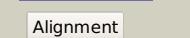
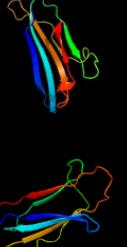
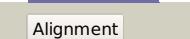
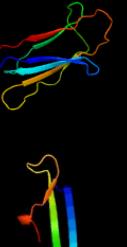
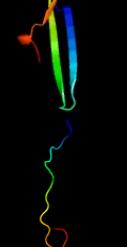
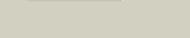
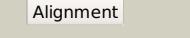
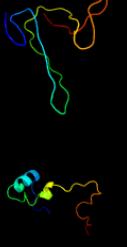
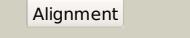
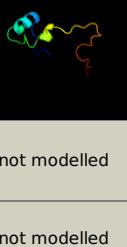
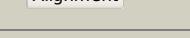
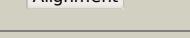
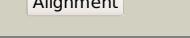


Phyre²

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Date	Tue Jul 23 14:50:47 BST 2019
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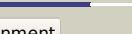
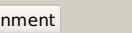
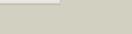
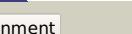
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lw3A	 Alignment		100.0	53	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmpps4; PDBTitle: solution structure of the soluble domain of mmpps4 from mycobacterium2 tuberculosis
2	d1fv1b1	 Alignment		50.6	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
3	d1dm1a1	 Alignment		37.5	19	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
4	d1muja1	 Alignment		35.0	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
5	d1zs8a1	 Alignment		33.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
6	d1d5mb1	 Alignment		29.0	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
7	d1uvqb1	 Alignment		28.4	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
8	c3osvC	 Alignment		26.2	7	PDB header: structural protein Chain: C: PDB Molecule: flagellar basal-body rod modification protein flgd; PDBTitle: the crytsal structure of flgd from p. aeruginosa
9	d1qqda1	 Alignment		26.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
10	d1c16a1	 Alignment		25.3	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
11	d1fnqb1	 Alignment		25.2	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)

12	c5lnkm_			21.8	32	PDB header: oxidoreductase Chain: M: PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i
13	d1uvqa1			20.1	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
14	d1klub1			20.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
15	d1mhca1			19.8	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
16	d1es0b1			19.3	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
17	c1dmIG_			19.1	19	PDB header: dna binding protein/transferase Chain: G: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of 2 hsv pol
18	c2kvzA_			18.7	41	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ispe; PDBTitle: structure of residues 161-235 of putative peptidoglycan binding2 protein lmo0835 from listeria monocytogenes: target lmr64b of the3 northeast structural genomics consortium
19	d1hx0a1			18.1	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
20	d1l3ga_			17.9	14	Fold: DNA-binding domain of Mlu1-box binding protein MBP1 Superfamily: DNA-binding domain of Mlu1-box binding protein MBP1 Family: DNA-binding domain of Mlu1-box binding protein MBP1
21	c2xkuA_		not modelled	17.1	14	PDB header: immune system Chain: A: PDB Molecule: beta-2-microglobulin; PDBTitle: prion-like conversion during amyloid formation at atomic resolution
22	d3d85d2		not modelled	17.0	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
23	c4ux5B_		not modelled	17.0	17	PDB header: transcription Chain: B: PDB Molecule: transcription factor mbp1; PDBTitle: structure of dna complex of pcg2
24	d1k8ib1		not modelled	16.5	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
25	d3dhpa1		not modelled	16.4	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
26	d1kska3		not modelled	16.2	36	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
27	d1neza1		not modelled	15.8	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
28	c1ywke_		not modelled	13.5	17	PDB header: isomerase Chain: E: PDB Molecule: 4-deoxy-l-threo-5-hexosulose-uronate ketol- PDBTitle: crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate 2 ketol-isomerase from enterococcus faecalis Fold: Immunoglobulin-like beta-sandwich

29	d1iaka1	Alignment	not modelled	13.5	11	Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
30	d1r3ha1	Alignment	not modelled	13.1	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
31	d1jk8a1	Alignment	not modelled	13.0	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
32	d1es0a1	Alignment	not modelled	13.0	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
33	c5lc5b_	Alignment	not modelled	12.8	32	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
34	d1kona_	Alignment	not modelled	12.7	35	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
35	c5o31b_	Alignment	not modelled	12.6	32	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: mitochondrial complex i in the deactive state
36	d1k8da1	Alignment	not modelled	12.5	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
37	d1a3xa1	Alignment	not modelled	12.5	15	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
38	d1lk2a1	Alignment	not modelled	12.4	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
39	c5e09A_	Alignment	not modelled	12.0	18	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
40	c2kncA_	Alignment	not modelled	11.9	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfa1b-beta3 transmembrane-cytoplasmic2 heterocomplex
41	d2iada1	Alignment	not modelled	11.9	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
42	d1kjva1	Alignment	not modelled	11.6	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
43	d1ywka1	Alignment	not modelled	11.5	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Kdul-like
44	d1x6oa2	Alignment	not modelled	11.1	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
45	c2amnA_	Alignment	not modelled	11.0	57	PDB header: antimicrobial protein Chain: A: PDB Molecule: cathelicidin; PDBTitle: solution structure of fowlcidin-1, a novel cathelicidin2 antimicrobial peptide from chicken
46	c5ldxb_	Alignment	not modelled	10.7	32	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class3.
47	c5ldwb_	Alignment	not modelled	10.7	32	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class1
48	c2na6A_	Alignment	not modelled	10.3	16	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
49	c2na6C_	Alignment	not modelled	10.3	16	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
50	c2na6B_	Alignment	not modelled	10.3	16	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
51	c5ee2A_	Alignment	not modelled	10.2	38	PDB header: metal transport Chain: A: PDB Molecule: hemoglobin-haptoglobin-utilization protein; PDBTitle: the crystal structure of the c-terminal beta-barrel of hpu4 from neisseria gonorrhoeae
52	d1k5na1	Alignment	not modelled	10.2	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
53	c1q40C_	Alignment	not modelled	9.9	33	PDB header: translation Chain: C: PDB Molecule: mRNA transport regulator mtr2; PDBTitle: crystal structure of the c. albicans mtr2-mex67 m domain complex
54	c5t9gD_	Alignment	not modelled	9.8	17	PDB header: hydrolase Chain: D: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2cwt in complex with galactosidofagomine PDB header: transcription

55	c4f3qA_	Alignment	not modelled	9.2	28	Chain: A: PDB Molecule: transcriptional regulatory protein cbu_1566; PDBTitle: structure of a yebc family protein (cbu_1566) from coxiella burnetii
56	d2fa8a1	Alignment	not modelled	9.2	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
57	d1s9va1	Alignment	not modelled	9.2	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
58	d1xtda2	Alignment	not modelled	9.0	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
59	c2jp3A_	Alignment	not modelled	9.0	10	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
60	d1xrual	Alignment	not modelled	9.0	38	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Kdul-like
61	d1jaea1	Alignment	not modelled	8.9	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
62	d1dgja2	Alignment	not modelled	8.8	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
63	c2obkE	Alignment	not modelled	8.7	32	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: selt/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
64	c6ansD_	Alignment	not modelled	8.6	41	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia cenocepacia
65	d1mw7a_	Alignment	not modelled	8.6	13	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
66	c5aeoA_	Alignment	not modelled	8.5	21	PDB header: immune system Chain: A: PDB Molecule: r. equi vapg protein; PDBTitle: virulence-associated protein vapg from the intracellular pathogen rhodococcus equi
67	c2kppA_	Alignment	not modelled	8.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0431 protein; PDBTitle: solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
68	d1vlba2	Alignment	not modelled	8.2	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
69	c2pnccB	Alignment	not modelled	7.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase, liver isozyme; PDBTitle: crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
70	d1liua1	Alignment	not modelled	7.9	18	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
71	c2lxFA_	Alignment	not modelled	7.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target gilaa.01396.a
72	d1of5b_	Alignment	not modelled	7.7	33	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
73	d1eg3a3	Alignment	not modelled	7.7	19	Fold: WW domain-like Superfamily: WW domain Family: WW domain
74	d1wbxa1	Alignment	not modelled	7.5	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
75	d1pkla1	Alignment	not modelled	7.5	23	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
76	c2yxyA_	Alignment	not modelled	7.5	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein, gk0453; PDBTitle: crystal structure of hypothetical conserved protein, gk0453
77	d1g94a1	Alignment	not modelled	7.1	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
78	d1dn0b2	Alignment	not modelled	7.0	6	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
79	c3owrA_	Alignment	not modelled	7.0	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized hypothetical protein; PDBTitle: crystal structure of a putative secreted protein (bf4250) from2 bacteroides fragilis nctc 9343 at 1.81 a resolution
80	d1vgka1	Alignment	not modelled	7.0	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
						PDB header: immune system

81	c3rolA_		Alignment	not modelled	6.9	15	Chain: A: PDB Molecule: h-2 class i histocompatibility antigen, k-b alpha chain; PDBTitle: murine class i major histocompatibility complex h-2kb in complex with post-translationally modified lcmv-derived gp34-41 peptide,3 comprising a nitrotyrosine at position 3
82	d1lfpa_		Alignment	not modelled	6.8	16	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
83	d1fnnga1		Alignment	not modelled	6.7	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
84	d1klua1		Alignment	not modelled	6.6	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
85	d3bzfa1		Alignment	not modelled	6.6	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
86	d1ok0a_		Alignment	not modelled	6.6	16	Fold: alpha-Amylase inhibitor tandemstat Superfamily: alpha-Amylase inhibitor tandemstat Family: alpha-Amylase inhibitor tandemstat
87	d1rm6c2		Alignment	not modelled	6.4	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
88	c4gdza_		Alignment	not modelled	6.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4251 family protein (bacegg_02002) from2 bacteroides eggerthii dsm 20697 at 1.95 a resolution
89	c6b6IB_		Alignment	not modelled	6.4	11	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, sugar binding domain protein; PDBTitle: the crystal structure of glycosyl hydrolase family 2 (gh2) member from2 bacteroides cellulosilyticus dsm 14838
90	c2p0gB_		Alignment	not modelled	6.4	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from vibrio2 cholerae. northeast structural genomics target vcr75
91	c4kw3A_		Alignment	not modelled	6.3	18	PDB header: viral protein Chain: A: PDB Molecule: ns1; PDBTitle: crystal structure of the non-structural protein 1 n-terminal origin-2 recognition/nickase domain from the emerging human bocavirus
92	d2rb6a1		Alignment	not modelled	6.3	22	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Ygdl/YgdR-like
93	c4gu8G_		Alignment	not modelled	6.2	22	PDB header: sugar binding protein Chain: G: PDB Molecule: b Burkholderia oklahomensis agglutinin (boa); PDBTitle: crystal structure of burkholderia oklahomensis agglutinin (boa)
94	c2kt7A_		Alignment	not modelled	6.2	25	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: putative peptidoglycan bound protein (lpxtg) PDBTitle: solution nmr structure of mucin-binding domain of protein2 Imo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
95	d1u8ib2		Alignment	not modelled	5.9	6	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
96	d1n62a2		Alignment	not modelled	5.8	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
97	d1t3qa2		Alignment	not modelled	5.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
98	c2kerA_		Alignment	not modelled	5.7	23	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-amylase inhibitor z-2685; PDBTitle: alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus
99	d2cs4a1		Alignment	not modelled	5.7	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD